OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/828,344

DATE: 04/27/2001
TIME: 12:43:29

Input Set : A:\RTS-0147 Sequence Listing.txt
Output Set: N:\CRF3\04272001\I828344.raw

```
   3 <110> APPLICANT: C. Frank Bennett
   4        Jacqueline Wyatt
   6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
   8 <130> FILE REFERENCE: RTS-0147
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/828,344
C--> 10 <141> CURRENT FILING DATE: 2001-04-06
  10 <160> NUMBER OF SEQ ID NOS: 176
  13 <210> SEQ ID NO: 1
  14 <211> LENGTH: 20
  15 <212> TYPE: DNA
  16 <213> ORGANISM: Artificial Sequence
  18 <220> FEATURE:
  20 <223> OTHER INFORMATION: Antisense Oligonucleotide
  22 <400> SEQUENCE: 1                                                 20
  23 tccgtcatcg ctcctcaggg
  26 <210> SEQ ID NO: 2
  27 <211> LENGTH: 20
  28 <212> TYPE: DNA
  29 <213> ORGANISM: Artificial Sequence
  31 <220> FEATURE:
  33 <223> OTHER INFORMATION: Antisense Oligonucleotide
  35 <400> SEQUENCE: 2                                                 20
  36 atgcattctg cccccaagga
  39 <210> SEQ ID NO: 3
  40 <211> LENGTH: 2077
  41 <212> TYPE: DNA
  42 <213> ORGANISM: Homo sapiens
  44 <220> FEATURE:
  46 <220> FEATURE:
  47 <221> NAME/KEY: CDS
  48 <222> LOCATION: (257)...(1213)
  50 <400> SEQUENCE: 3
  51 ccgagcgcca gcgcggggaa ccgggaaaag gaaaccgtgt tgtgtacgta agattcagga    60
  53 aacgaaacca ggagccgcgg gtgttggcgc aaaggttact cccagaccct tttccggctg   120
  55 acttctgaga aggttgcgca cagctgtgcc cggcagtcta gaggcgcaga agaggaagcc   180
  57 atcgcctggc cccggctctc tggaccttgt ctcgctcggg agcggaaaca gcggcagcca   240
  59 gagaactgtt ttaatc atg gac aaa caa aac tca cag atg aat gct tct cac   292
  60                     Met Asp Lys Gln Asn Ser Gln Met Asn Ala Ser His
  61                      1               5                  10
  63 ccg gaa aca aac ttg cca gtt ggg tat cct cct cag tat cca ccg aca    340
  64 Pro Glu Thr Asn Leu Pro Val Gly Tyr Pro Pro Gln Tyr Pro Pro Thr
  65          15                  20                  25
  67 gca ttc caa gga cct cca gga tat agt ggc tac cct ggg ccc cag gtc    388
  68 Ala Phe Gln Gly Pro Pro Gly Tyr Ser Gly Tyr Pro Gly Pro Gln Val
  69          30                  35                  40
  71 agc tac cca ccc cca cca gcc ggc cat tca ggt cct ggc cca gct ggc    436
  72 Ser Tyr Pro Pro Pro Pro Ala Gly His Ser Gly Pro Gly Pro Ala Gly
```

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                              50                       55              60
73  45                                                                        484
75  ttt cct gtc cca aat cag cca gtg tat aat cag cca gta tat aat cag
76  Phe Pro Val Pro Asn Gln Pro Val Tyr Asn Gln Pro Val Tyr Asn Gln
77              65                       70                  75
79  cca gtt gga gct gca ggg gta cca tgg atg cca gcg cca cag cct cca        532
80  Pro Val Gly Ala Ala Gly Val Pro Trp Met Pro Ala Pro Gln Pro Pro
81              80                       85                  90
83  tta aac tgt cca cct gga tta gaa tat tta agt cag ata gat cag ata        580
84  Leu Asn Cys Pro Pro Gly Leu Glu Tyr Leu Ser Gln Ile Asp Gln Ile
85          95                      100                 105
87  ctg att cat cag caa att gaa ctt ctg gaa gtt tta aca ggt ttt gaa        628
88  Leu Ile His Gln Gln Ile Glu Leu Leu Glu Val Leu Thr Gly Phe Glu
89      110                     115                 120
91  act aat aac aaa tat gaa att aag aac agc ttt gga cag agg gtt tac        676
92  Thr Asn Asn Lys Tyr Glu Ile Lys Asn Ser Phe Gly Gln Arg Val Tyr
93  125                     130                 135                 140
95  ttt gca gcg gaa gat act gat tgc tgt acc cga aat tgc tgt ggg cca        724
96  Phe Ala Ala Glu Asp Thr Asp Cys Cys Thr Arg Asn Cys Cys Gly Pro
97              145                     150                 155
99  tct aga cct ttt acc ttg agg att att gat aat atg ggt caa gaa gtc        772
100 Ser Arg Pro Phe Thr Leu Arg Ile Ile Asp Asn Met Gly Gln Glu Val
101             160                     165                 170
103 ata act ctg gag aga cca cta aga tgt agc agc tgt tgt tgt ccc tgc        820
104 Ile Thr Leu Glu Arg Pro Leu Arg Cys Ser Ser Cys Cys Cys Pro Cys
105         175                     180                 185
107 tgc ctt cag gag ata gaa atc caa gct cct cct ggt gta cca ata ggt        868
108 Cys Leu Gln Glu Ile Glu Ile Gln Ala Pro Pro Gly Val Pro Ile Gly
109     190                     195                 200
111 tat gtt att cag act tgg cac cca tgt cta cca aag ttt aca att caa        916
112 Tyr Val Ile Gln Thr Trp His Pro Cys Leu Pro Lys Phe Thr Ile Gln
113 205                     210                 215                 220
115 aat gag aaa aga gag gat gta cta aaa ata agt ggt cca tgt gtt gtg        964
116 Asn Glu Lys Arg Glu Asp Val Leu Lys Ile Ser Gly Pro Cys Val Val
117             225                     230                 235
119 tgc agc tgt tgt gga gat gtt gat ttt gag att aaa tct ctt gat gaa        1012
120 Cys Ser Cys Cys Gly Asp Val Asp Phe Glu Ile Lys Ser Leu Asp Glu
121             240                     245                 250
123 cag tgt gtg gtt ggc aaa att tcc aag cac tgg act gga att ttg aga        1060
124 Gln Cys Val Val Gly Lys Ile Ser Lys His Trp Thr Gly Ile Leu Arg
125         255                     260                 265
127 gag gca ttt aca gac gct gat aac ttt gga atc cag ttc cct tta gac        1108
128 Glu Ala Phe Thr Asp Ala Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp
129     270                     275                 280
131 ctt gat gtt aaa atg aaa gct gta atg att ggt gcc tgt ttc ctc att        1156
132 Leu Asp Val Lys Met Lys Ala Val Met Ile Gly Ala Cys Phe Leu Ile
133 285                     290                 295                 300
135 gac ttc atg ttt ttt gaa agc act ggc agc cag gaa caa aaa tca gga        1204
136 Asp Phe Met Phe Phe Glu Ser Thr Gly Ser Gln Glu Gln Lys Ser Gly
137             305                     310                 315
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139 gtg tgg tag tggattagtg aaagtctcct caggaaatct gaagtctgta tattgattga 1263
140 Val Trp
143 gactatctaa actcatacct gtatgaatta agctgtaagg cctgtagctc tggttgtata 1323
145 cttttgcttt tcaaattata gtttatcttc tgtataactg atttataaag gttttttgtac 1383
147 attttttaat actcattgtc aatttgagaa aaaggacata tgagtttttg catttattaa 1443
149 tgaaacttcc tttgaaaaac tgctttgaat tatgatctct gattcattgt ccattttact 1503
151 accaaatatt aactaaggcc ttattaattt ttatatgttatt tatatcttgt cctattaaat 1563
151 accaaatatt aactaaggcc ttattaattt ttatatgttatt ttgcaaatgc catatattca 1623
153 ctagttacaa tttatttcat gcataagagc taatgttatt ttgcaaatgc catatattca 1623
155 aaaaagctca aagataattt tctttactat tatgttcaaa taatattcaa tatgcatatt 1683
157 atctttaaaa agttaaatgt tttttttaatc ttcaagaaat catgctacac ttaacttctc 1743
159 ctagaagcta atctatacca taatattttc atattcacaa gatattaaat taccaatttt 1803
161 caaattattg ttagtaaaga acaaaatgat tctctcccaa agaaagacac attttaaata 1863
163 ctccttcact ctaaaactct ggtattataa cttttgaaag ttaatatttc tacatgaaat 1923
165 gtttagctct tacactctat ccttcctaga aaatggtaat tgagattact cagatattaa 1983
167 ttaaatacaa tatcatatat atattcacag agtataaacc taaataatga tctattagat 2043
169 tcaaatattt gaaataaaaa cttgattttt ttgt                               2077
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172 <210> SEQ ID NO: 4
173 <211> LENGTH: 16
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
179 <223> OTHER INFORMATION: PCR Primer
181 <400> SEQUENCE: 4                                                   16
182 cgggtgttgg cgcaaa
185 <210> SEQ ID NO: 5
186 <211> LENGTH: 20
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
192 <223> OTHER INFORMATION: PCR Primer
194 <400> SEQUENCE: 5                                                   20
195 ctgtgcgcaa ccttctcaga
198 <210> SEQ ID NO: 6
199 <211> LENGTH: 26
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
205 <223> OTHER INFORMATION: PCR Probe
207 <400> SEQUENCE: 6                                                   26
208 ttactcccag acccttttcc ggctga
211 <210> SEQ ID NO: 7
212 <211> LENGTH: 19
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
218 <223> OTHER INFORMATION: PCR Primer
220 <400> SEQUENCE: 7                                                   19
221 gaaggtgaag gtcggagtc
224 <210> SEQ ID NO: 8
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225 <211> LENGTH: 20
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
231 <223> OTHER INFORMATION: PCR Primer
233 <400> SEQUENCE: 8                                                    20
234 gaagatggtg atgggatttc
237 <210> SEQ ID NO: 9
238 <211> LENGTH: 20
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
244 <223> OTHER INFORMATION: PCR Probe
246 <400> SEQUENCE: 9                                                    20
247 caagcttccc gttctcagcc
250 <210> SEQ ID NO: 10
251 <211> LENGTH: 1622
252 <212> TYPE: DNA
253 <213> ORGANISM: Mus musculus
255 <220> FEATURE:
257 <220> FEATURE:
258 <221> NAME/KEY: CDS
259 <222> LOCATION: (192)...(1115)
261 <400> SEQUENCE: 10
262 tctaaagact caggaaacaa aacctaaatt gcctcaaagt tcaggtgctt tttctccctg    60
264 actttagtct agtggagtag tgcagcacct atgcctttct gagaggagtc tggagagctg   120
266 agtcgctgct ggtgctagga ttctaggaat tcgcctcact tggagctgca tgagaaaaga   180
268 aaggcttgca a atg gag gct cct cgc tca gga aca tac ttg cca gct ggg   230
269                  Met Glu Ala Pro Arg Ser Gly Thr Tyr Leu Pro Ala Gly
270                   1               5                  10
272 tat gcc cct cag tat cct cca gca gca gtc caa gga cct cca gag cat   278
273 Tyr Ala Pro Gln Tyr Pro Pro Ala Ala Val Gln Gly Pro Pro Glu His
274         15                  20                  25
276 act gga cgc ccc aca ttc cag act aac tac caa gtt ccc cag tct ggt   326
277 Thr Gly Arg Pro Thr Phe Gln Thr Asn Tyr Gln Val Pro Gln Ser Gly
278  30                  35                  40                  45
280 tat cca gga cct cag gct agc tac aca gtc tca aca tct gga cat gaa   374
281 Tyr Pro Gly Pro Gln Ala Ser Tyr Thr Val Ser Thr Ser Gly His Glu
282                  50                  55                  60
284 ggt tat gct gct aca cgg ctt cct att caa aat aat cag act ata gtc   422
285 Gly Tyr Ala Ala Thr Arg Leu Pro Ile Gln Asn Asn Gln Thr Ile Val
286             65                  70                  75
288 ctt gca aac act cag tgg atg cca gca cca cca cct att ctg aac tgc   470
289 Leu Ala Asn Thr Gln Trp Met Pro Ala Pro Pro Pro Ile Leu Asn Cys
290         80                  85                  90
292 cca cct ggg cta gaa tac tta aat cag ata gat cag ctt ctg att cat   518
293 Pro Pro Gly Leu Glu Tyr Leu Asn Gln Ile Asp Gln Leu Leu Ile His
294         95                 100                 105
296 cag caa gtt gaa ctt cta gaa gtc tta aca ggc ttt gaa aca aat aac   566
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297 Gln Gln Val Glu Leu Leu Glu Val Leu Thr Gly Phe Glu Thr Asn Asn
298 110                 115                 120                 125
300 aaa ttt gaa atc aag aac agc ctc ggg cag atg gtt tat gtt gca gtg      614
301 Lys Phe Glu Ile Lys Asn Ser Leu Gly Gln Met Val Tyr Val Ala Val
302                 130                 135                 140
304 gaa gat act gac tgc tgt act cga aat tgc tgt gaa gcg tct aga cct      662
305 Glu Asp Thr Asp Cys Cys Thr Arg Asn Cys Cys Glu Ala Ser Arg Pro
306             145                 150                 155
308 ttc acc tta aga atc ctg gat cat ctg ggc caa gaa gtc atg act ctg      710
309 Phe Thr Leu Arg Ile Leu Asp His Leu Gly Gln Glu Val Met Thr Leu
310         160                 165                 170
312 gag cga cct ctg aga tgc agt agc tgc tgc ttc ccc tgc tgc ctc cag      758
313 Glu Arg Pro Leu Arg Cys Ser Ser Cys Cys Phe Pro Cys Cys Leu Gln
314         175                 180                 185
316 gag ata gaa atc cag gct cct ccg ggg gtg cca ata ggt tat gtg act      806
317 Glu Ile Glu Ile Gln Ala Pro Pro Gly Val Pro Ile Gly Tyr Val Thr
318 190                 195                 200                 205
320 cag acc tgg cac cca tgt ctg cca aag ctc act ctt cag aac gac aag      854
321 Gln Thr Trp His Pro Cys Leu Pro Lys Leu Thr Leu Gln Asn Asp Lys
322             210                 215                 220
324 agg gag aat gtt cta aaa gta gtt ggt cca tgt gtt gca tgc acc tgc      902
325 Arg Glu Asn Val Leu Lys Val Val Gly Pro Cys Val Ala Cys Thr Cys
326             225                 230                 235
328 tgt tca gat att gac ttt gag atc aag tct ctt gat gaa gtg act aga      950
329 Cys Ser Asp Ile Asp Phe Glu Ile Lys Ser Leu Asp Glu Val Thr Arg
330         240                 245                 250
332 att ggt aag atc acc aag cag tgg tct ggt tgt gtg aaa gag gcc ttc      998
333 Ile Gly Lys Ile Thr Lys Gln Trp Ser Gly Cys Val Lys Glu Ala Phe
334         255                 260                 265
336 acg gat tcg gat aac ttt ggg atc caa ttc ccg cta gac ctg gag gtg      1046
337 Thr Asp Ser Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp Leu Glu Val
338 270                 275                 280                 285
340 aag atg aaa gct gtg acg ctt ggt gct tgc ttc ctc ata gat tac atg      1094
341 Lys Met Lys Ala Val Thr Leu Gly Ala Cys Phe Leu Ile Asp Tyr Met
342             290                 295                 300
344 ttt ttt gaa ggc tgt gag tag gaacagaaat ccgacctgca gtaggaatca         1145
345 Phe Phe Glu Gly Cys Glu
346             305
348 atgaaagagg acagagaaga tctgaagtct acacaaggag atcatatgat tgagagacct    1205
350 ggggcttttt gatttcttca ttgaaatttc tcagaatcaa gctgttatac atgaagcata    1265
352 gtatgtaaca ttttggtttt caaatggtag tttatctttt acattattgg aatagacctg    1325
354 gataattatc tttatacact tctaaaaata tgcaccaaat tcaagttaaa aaaaaaaga     1385
356 cgaagagaag tgtatgtttt aaaataaaac attttatgga aaagtaagtt aaatcataat    1445
358 ctgggattta ttttttcatct tttgttcaat ttaaaccttg ttagtgctga ttttattata   1505
360 aaattgtact ttactatcaa acctagttag tttatttctt acagaaatcc tcctattatt    1565
362 ttgaaattac atattttga aagctttta aaagatacta ttgcctggga aattcta         1622
365 <210> SEQ ID NO: 11
366 <211> LENGTH: 21
367 <212> TYPE: DNA
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

4/27/01

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/828,344

DATE: 04/27/2001
TIME: 12:43:30

Input Set : **A:\RTS-0147 Sequence Listing.txt**
Output Set: **N:\CRF3\04272001\I828344.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18